Amendments to the Specification

Please replace the paragraph at page 7, line 19 through page 8, line 7 with the following amended paragraph:

Figure 2 shows the multiple sequence alignment with IκBNS (SEQ ID NO: 4). The full sequence of IκBNS is shown. Numbering refers to IκBNS. The ankyrin domains of IκBNS are boxed and labeled from A to G. Secondary structure (ss) predictions for IκBNS are shown above the alignment with the inner helix of the ankyrin repeat core shown in gray, and the outer in blue. Secondary structure motifs of IκBα were obtained from pdb 1NFI (Jacobs and Harrison, 1998) and are shown below the alignment. Sequences were aligned using the program ClustalX (Thompson *et al.,* 1997), and the secondary structure prediction of IκBNS was determined using PSI-PRED (Jones, 1999). A dendrogram of the figure is displayed with IκBα as the root and was derived using the Neighborjoining method (Saitou and Nei, 1987). Amino acid positions with identities or similarities in 5 or more of the 6 proteins aligned are highlighted in black with yellow letters. Amino acid positions with identities or similarities in four or more of the 6 proteins are highlighted in gray. For this analysis, V/L/I, S/T, N/Q, D/E, K/R and W/F are considered equal. Residues shown are: for human IκBα aa 66-287 (SEQ ID NO: 12), for human Bcl-3 aa 31-278 (SEQ ID NO: 9), for murine IκBζ aa 292-629 (SEQ ID NO: 8), for human p105 aa 522-756 (SEQ ID NO: 11) and for murine p100 aa 467-705 (SEQ ID NO: 10).

Please replace the paragraph at page 43, lines 17 through 26 with the following amended paragraph:

FTOC were set up as described. On day 4, phosphorothioate oligonucleotides (sense, 5'CCCCTGGTGATGGAGGACTCT3' (SEQ ID NO: 6), or antisense, 5'AGAGTCCTCCATCACCAGGGG3' (SEQ ID NO: 7) from MWG Biotech, Inc.) were added at 200 μg/ml. After 12-19 h, VSV8 peptide was added to some FTOC at 300 μM. After 4 more hours, thymic lobes were harvested and analyzed by FACS. Thymocytes were stained at ~5 x 10^6

cells per ml in PBS-2% FCS-0.05% NaN3 containing the antibodies at saturating concentrations. The antibodies were anti-CD8α-FITC (53-6.7) and anti-CD4-PE (RM4.5) from Pharmingen. The phenotypes and proportions of thymocyte subsets were analyzed by two-color flow cytometry using a FACScan (Becton Dickinson) and the CellQuest program. Dead cells were excluded by gating.